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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=10; day=30; hr=15; min=43; sec=55; ms=230;  
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Application No: 10527973 Version No: 1.0

Input Set:

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Finished: 2008-09-24 11:29:39.226  
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Total Errors: 0  
No. of SeqIDs Defined: 7  
Actual SeqID Count: 7

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# SEQUENCE LISTING

<110> Lingappa, Jairam  
 Lingappa, Jaisri  
 Lingappa, Vishwanath

<120> Viral Deconstruction Through Capsid Assembly In Vitro

<130> 305JP-010510US

<140> 10527973  
 <141> 2008-09-24

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<170> PatentIn version 3.5

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Lys Thr Gly Lys Leu Cys Ile Glu Val Ser Pro Val Ala Lys Leu Ala  
 35 40 45

Phe Ile Ser Glu Glu Leu Cys Ile Gly Cys Gly Ile Cys Val Lys Lys  
 50 55 60

Cys Pro Phe Asp Ala Ile Glu Ile Ile Asn Leu Pro Lys Asp Leu Glu  
 65 70 75 80

Lys Asp Thr Thr His Arg Tyr Gly Pro Asn Thr Phe Lys Leu His Arg  
 85 90 95

Leu Pro Val Pro Arg Pro Gly Gln Val Leu Gly Leu Val Gly Thr Asn  
 100 105 110

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Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Arg Ile Leu		
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Glu Asp Asn Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Asp His Ile		
165	170	175
Pro Lys Ala Val Gln Gly Asn Val Gly Gln Val Leu Glu Gln Lys Asp		
180	185	190
Glu Arg Asp Met Lys Asn Glu Leu Cys Val Asp Leu Glu Leu Asn Gln		
195	200	205
Val Ile Asp Arg Asn Val Gly Asp Leu Ser Gly Gly Glu Leu Gln Arg		
210	215	220
Phe Ala Ile Ala Val Val Ala Val Gln Ser Ala Glu Ile Tyr Met Phe		
225	230	235 240
Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala		
245	250	255
Arg Val Ile Arg Ser Leu Leu Arg Ser Asn Ser Tyr Val Ile Val Val		
260	265	270
Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys		
275	280	285
Leu Tyr Gly Lys Pro Gly Ala Tyr Gly Val Val Thr Leu Pro Phe Ser		
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Val Arg Glu Gly Ile Asn Ile Phe Leu Ala Gly Phe Val Pro Thr Glu		
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Asn Leu Arg Phe Arg Asp Glu Ser Leu Thr Phe Lys Ile Ala Glu Thr		
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Gln Glu Ser Ala Glu Glu Val Ala Thr Tyr Gln Arg Tyr Lys Tyr Pro  
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355 360 365

Glu Phe Thr Asp Ser Gln Ile Val Val Met Leu Gly Glu Asn Gly Thr  
370 375 380

Gly Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Leu Leu Lys Pro Asp  
385 390 395 400

Thr Met Glu Gly Thr Glu Val Glu Ile Pro Glu Phe Asn Val Ser Tyr  
405 410 415

Lys Pro Gln Lys Ile Ser Pro Lys Phe Gln His Pro Val Arg His Leu  
420 425 430

Leu His Ser Lys Ile Arg Asp Ser Tyr Thr His Pro Gln Phe Val Ser  
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Asp Val Met Lys Pro Leu Gln Ile Glu Gln Leu Met Asp Gln Glu Val  
450 455 460

Ile Asn Leu Ser Gly Gly Glu Leu Gln Arg Val Ala Leu Cys Leu Cys  
465 470 475 480

Leu Gly Lys Pro Ala Asp Ile Tyr Leu Ile Asp Glu Pro Ser Ala Tyr  
485 490 495

Leu Asp Ser Glu Gln Arg Ile Val Ala Ser Lys Val Ile Lys Arg Phe  
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Ile Leu His Ala Lys Lys Thr Ala Phe Ile Val Glu His Asp Phe Ile  
515 520 525

Met Ala Thr Tyr Leu Ala Asp Lys Val Ile Val Tyr Glu Gly Leu Ala  
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Ser Ile Asp Cys Thr Ala Asn Ala Pro Gln Ser Leu Val Ser Gly Met  
545 550 555 560

Asn Lys Phe Leu Ser His Leu Asp Ile Thr Phe Arg Arg Asp Pro Thr



565

570

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<212> PRT

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 35 40 45

Trp Ile Ser Glu Thr Leu Cys Ile Gly Cys Gly Ile Cys Ile Lys Lys  
 50 55 60

Cys Pro Phe Gly Ala Leu Ser Ile Val Asn Leu Pro Ser Asn Leu Glu  
 65 70 75 80

Lys Glu Thr Thr His Arg Tyr Cys Ala Asn Ala Phe Lys Leu His Arg  
 85 90 95

Leu Pro Ile Pro Arg Pro Gly Glu Val Leu Gly Leu Val Gly Thr Asn  
 100 105 110

Gly Ile Gly Lys Ser Thr Ala Leu Lys Ile Leu Ala Gly Lys Gln Lys  
 115 120 125

Pro Asn Leu Gly Lys Tyr Asp Asp Pro Pro Asp Trp Gln Glu Ile Leu  
 130 135 140

Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Lys Ile Leu  
 145 150 155 160

Glu Asp Asp Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Asp Gln Ile		
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Pro Lys Ala Ala Lys Gly Thr Val Gly Ser Ile Leu Asp Arg Lys Asp		
180	185	190
Glu Thr Lys Thr Gln Ala Ile Val Cys Gln Gln Leu Asp Leu Thr His		
195	200	205
Leu Lys Glu Arg Asn Val Glu Asp Leu Ser Gly Gly Glu Leu Gln Arg		
210	215	220
Phe Ala Cys Ala Val Val Cys Ile Gln Lys Ala Asp Ile Phe Met Phe		
225	230	235 240
Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala		
245	250	255
Ile Thr Ile Arg Ser Leu Ile Asn Pro Asp Arg Tyr Ile Ile Val Val		
260	265	270
Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys		
275	280	285
Leu Tyr Gly Val Pro Ser Ala Tyr Gly Val Val Thr Met Pro Phe Ser		
290	295	300
Val Arg Glu Gly Ile Asn Ile Phe Leu Asp Gly Tyr Val Pro Thr Glu		
305	310	315 320
Asn Leu Arg Phe Arg Asp Ala Ser Leu Val Phe Lys Val Ala Glu Thr		
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Ala Asn Glu Glu Glu Val Lys Lys Met Cys Met Tyr Lys Tyr Pro Gly		
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Met Lys Lys Lys Met Gly Glu Phe Glu Leu Ala Ile Val Ala Gly Glu		
355	360	365
Phe Thr Asp Ser Glu Ile Met Val Met Leu Gly Glu Asn Gly Thr Gly		
370	375	380

Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Arg Leu Lys Pro Asp Glu  
385 390 395 400

Gly Gly Glu Val Pro Val Leu Asn Val Ser Tyr Lys Pro Gln Lys Ile  
405 410 415

Ser Pro Lys Ser Thr Gly Ser Val Arg Gln Leu Leu His Glu Lys Ile  
420 425 430

Arg Asp Ala Tyr Thr His Pro Gln Phe Val Thr Asp Val Met Lys Pro  
435 440 445

Leu Gln Ile Glu Asn Ile Ile Asp Gln Glu Val Gln Thr Leu Ser Gly  
450 455 460

Gly Glu Leu Gln Arg Val Ala Leu Ala Leu Cys Leu Gly Lys Pro Ala  
465 470 475 480

Asp Val Tyr Leu Ile Asp Glu Pro Ser Ala Tyr Leu Asp Ser Glu Gln  
485 490 495

Arg Leu Met Ala Ala Arg Val Val Lys Arg Phe Ile Leu His Ala Lys  
500 505 510

Lys Thr Ala Phe Val Val Glu His Asp Phe Ile Met Ala Thr Tyr Leu  
515 520 525

Ala Asp Arg Val Ile Val Phe Asp Gly Val Pro Ser Lys Asn Thr Val  
530 535 540

Ala Asn Ser Pro Gln Thr Leu Leu Ala Gly Met Asn Lys Phe Leu Ser  
545 550 555 560

Gln Leu Glu Ile Thr Phe Arg Arg Asp Pro Asn Asn Tyr Arg Pro Arg  
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Asn Tyr Phe Phe Leu Asp Asp  
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